NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]
x_dropoff: [30] expect: [10.00] wordsize: [3] Filter [] [Align]

Sequence 1 gi 4140289   Length 215 (1 .. 215)
Sequence 2 gi 123369 High mobility group protein 1 (HMG-1). Length 215 (1 .. 215)
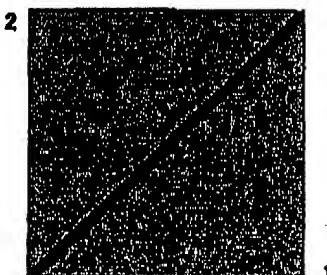
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 415 bits (1067), Expect = e-115
Identities = 195/215 (90%), Positives = 209/215 (96%)

```
Query:        1  MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSSKEKGKF 60
                 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMS+KEKGKF
Sbjct:        1  MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
dna-binding   9  **********************************************************
HMG1          1  +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:       61  EDMAKADKLRYEKEMKNYVPPKGETKKKFKDPNAPKRPPSAFFLFCSEFRPKIKGEHPGL 120
                 EDMAKADK RYE+EMK Y+PPKGETKKKFKDPNAPKRPPSAFFLFCSE+RPKIKGEHPGL
Sbjct:       61  EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
dna-binding  95  *****************
dna-binding  61  ******************
HMG1         61  +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:      121  SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKVDAGKKVVAKAEK 180
                 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGK DA KK V KAEK
Sbjct:      121  SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
dna-binding 121  **********************************************
HMG1        121  ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:      181  SKKKKEEEEDEDEDEEDEEDEEEEEEEEEDDDDDE 215
                 SKKKKEEEEDE+++E++EE+E+EE+E+EE+DDDDE
Sbjct:      181  SKKKKEEEEDEEDEEDEEEEEEDEEDEDEEEDDDDE 215
ASP/GLU-RICH (ACIDIC). 186  *******************************
HMG1        181  ++++++++++++++++++++++++++++++++++++
```

CPU time: 0.03 user secs.   0.06 sys. secs   0.09 total secs.

Lambda   K   H
   0.304   0.127   0.357

Gapped
Lambda   K   H
   0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 5441

EXHIBIT A

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr–24–2002]

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1
x_dropoff: 30 expect: 10.00 wordsize: 3 Filter ☐ Align

Sequence 1 gi 123373 High mobility group protein 2 (HMG–2). Length 207 (1 .. 207)
Sequence 2 gi 123374 High mobility group protein 2 (HMG–2). Length 209 (1 .. 209)
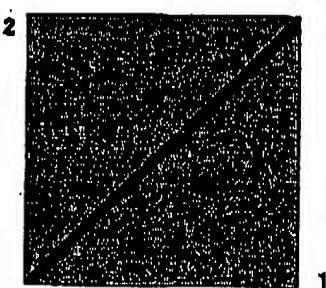
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 402 bits (1034), Expect = e–112
Identities = 188/207 (90%), Positives = 201/207 (96%)

```
Query:       1   MGKGDPNKPRGKMSSYAYFVQTCREEHKKKHPDSSVNFAEFSRKCSERWKTMSSKEKGKF 60
                 MGKGDPNKPRGKMSSYA+FVQTCREEHKKKHPDSSVNFAEFS+KCSERWKTMS+KEK KF
Sbjct:       1   MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 60
dna-binding  9   *********************************************************
HMG2         1   +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:      61   EEMAKGDKARYDREMKNYVPPKGEKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKNDHPGL 120
                 E+MAK DKARYDREMKNYVPPKG+KKGKKKDPNAPKRPPSAFFLFCSEHRPKIK++HPGL
Sbjct:      61   EDMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGL 120
dna-binding  95
dna-binding  61  *****************
HMG2         61  +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:     121   SIGDTAKKLGEMWSEQLAKDKQPYEQKAAKLKEKYEKDIAAYRAKSKSDAGKKGPGRPAG 180
                 SIGDTAKKLGEMWSEQ AKDKQPYEQKAAKLKEKYEKDIAAYRAK KS+AGKKGPGRP G
Sbjct:     121   SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTG 180
Conflict    163
dna-binding 121  ****************************************************
HMG2        121  +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++

Query:     181   SKKKAEPEEEEEEEEDEEEEEEEEDEE 207
                 SKKK EPE+EEEEEE+E+E+EEEEDE+
Sbjct:     181   SKKKNEPEDEEEEEEEEDEDEEEEDED 207
ASP/GLU-RICH (ACIDIC).  186  ********************
HMG2        181  ++++++++++++++++++++++
```

CPU time: 0.06 user secs.   0.03 sys. secs   0.09 total secs.

Lambda   K   H
  0.304   0.126   0.358

Gapped
Lambda   K   H
  0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1